

Shown is the 3'UTR of the human IL1B sequence from accession number M15330.

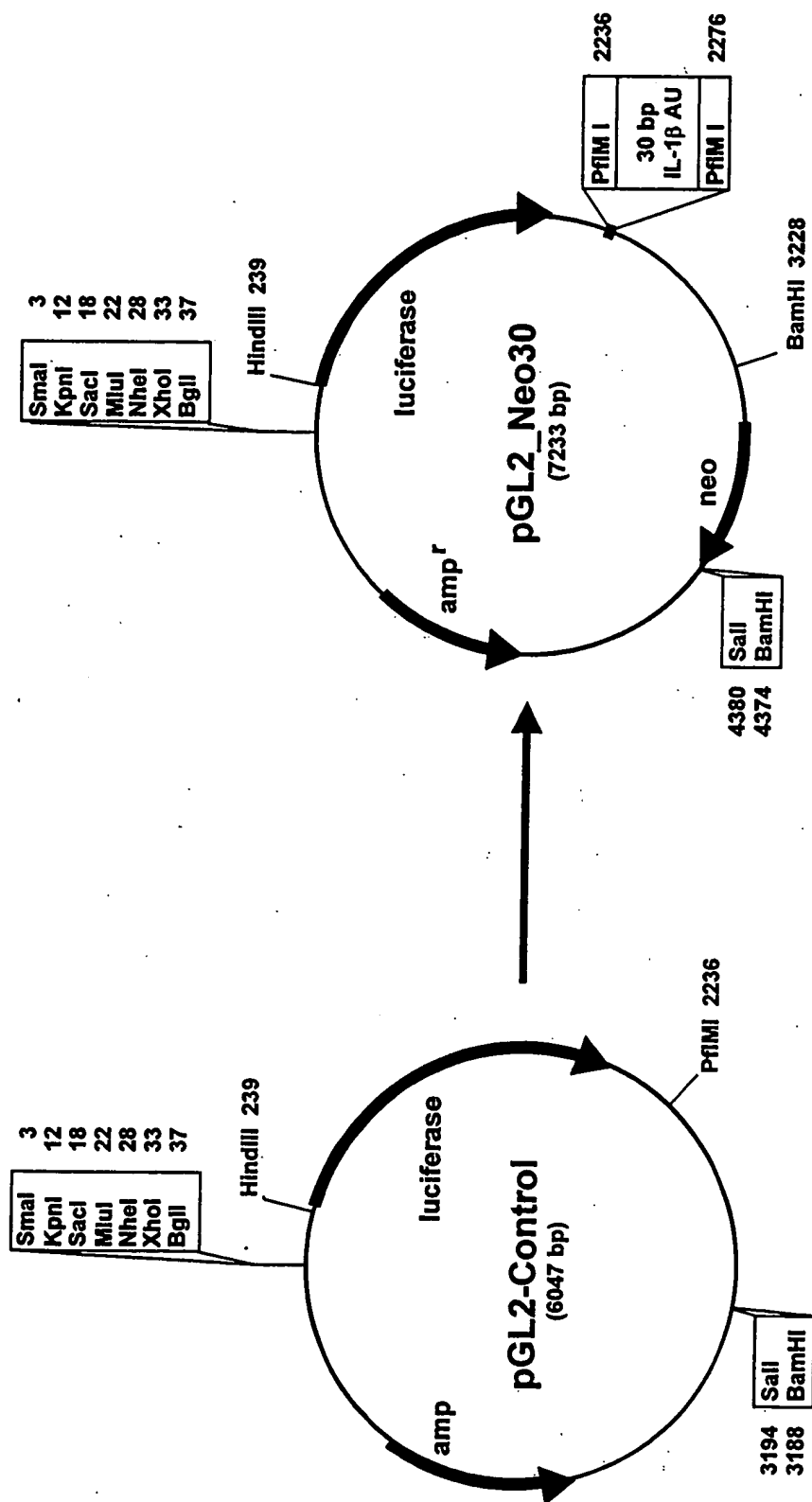
\* Represents the stop codon.

\*AGAGAGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCCTAG  
GGCTGGCAGAAAGGAACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGAC  
TTTCCTGTGTCTACACCAATGCCCCAACTGCCCTGCTTAGGGTAGTGCTAA  
GAGGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCC  
AATCCCAGCCCTTTTGTGAGCCAGGCTCTCTCACCTCTCCTACTCACT  
TAAAGCCCGCTGACAGAAACACGGCCACATTTGGTTCTAAGAAACCCCTC  
TGTCATTGCTCCACATTCTGATGAGCAACCGCTTCCCTATTTATTTATT  
TATTTGTTGTTTATTTATTTGTTGTTAATTTATTCAAGGGGCAAG  
AAGTAGCAGTGTCTGTAAAGAGCCTAGTTTTTAATAGCTATGGAATCAAT  
TCAATTGGACTGGTGTCTCTTTAAATCAAGTCCTTTAATTAAGACTG  
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TATCATACTGTTCAATGGTTCTGAAATAAACTTCTCTGAAG

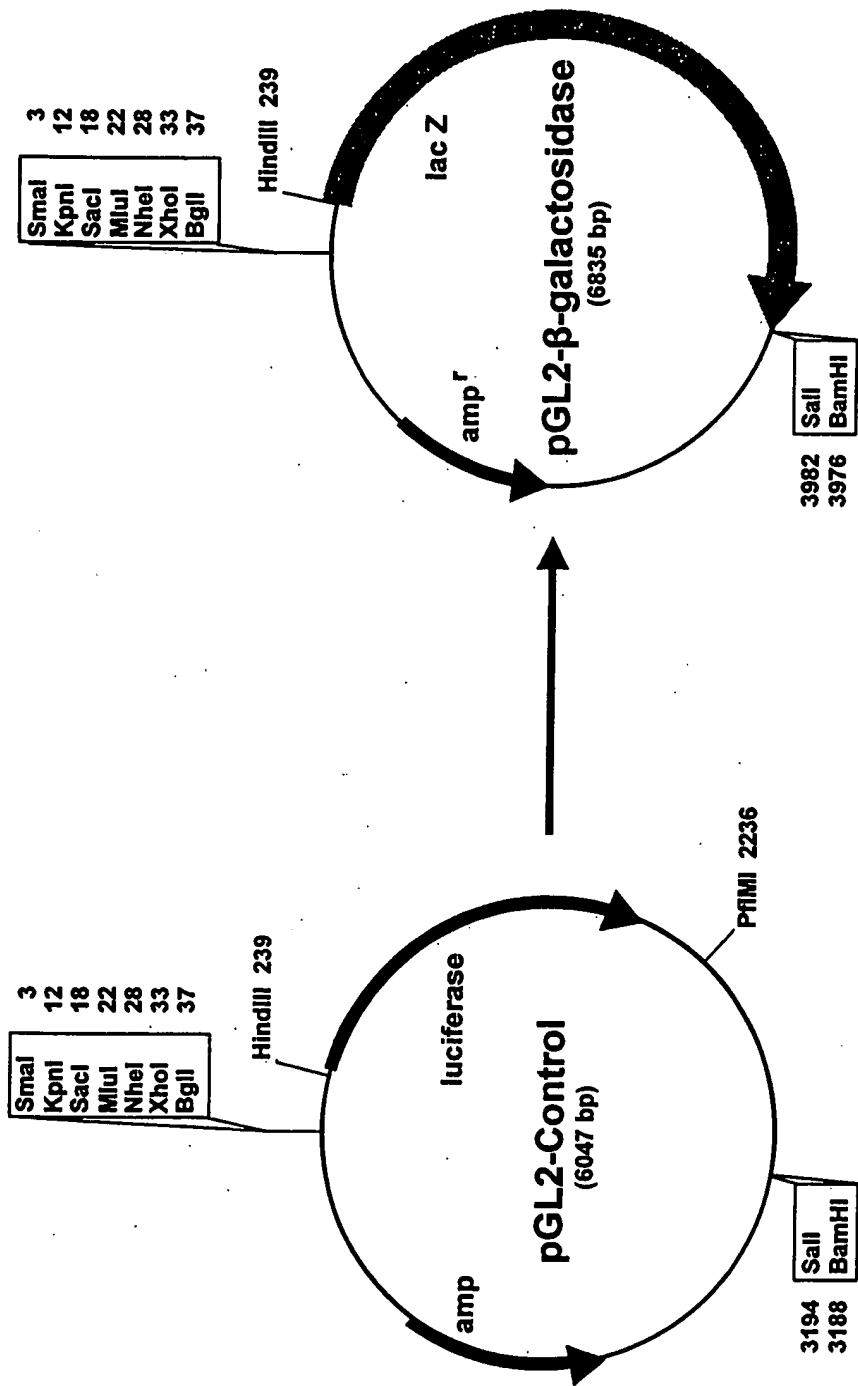
FIGURE 1

ATGGCTTCCCT**ATTATTTATTTATTT**TTGTTGTCCACCT  
|||||  
GGATACCGAAGG**ATAATAATAATA**TAACAAACAGGTT

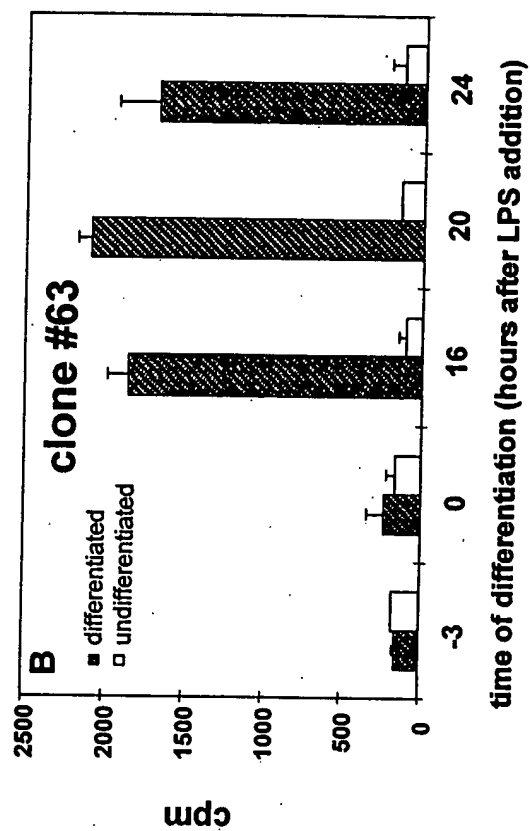
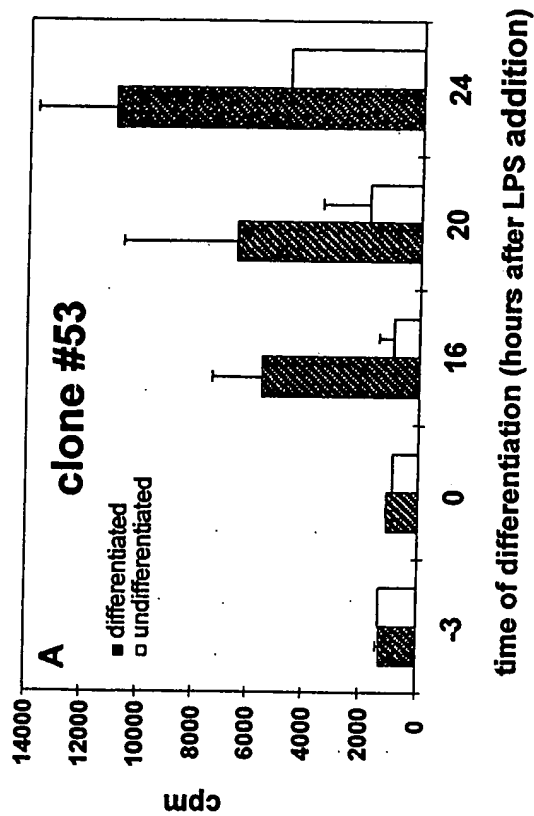
**FIGURE 2**



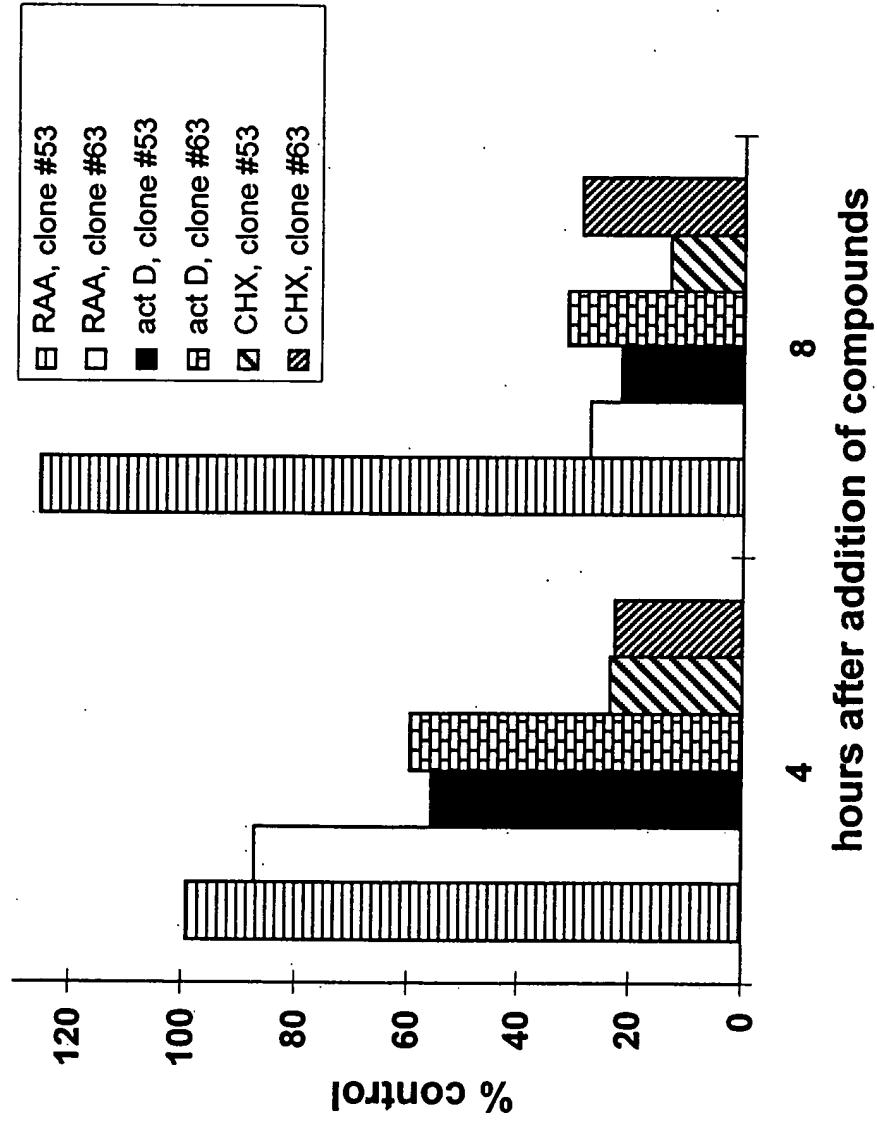
**FIGURE 3 A**



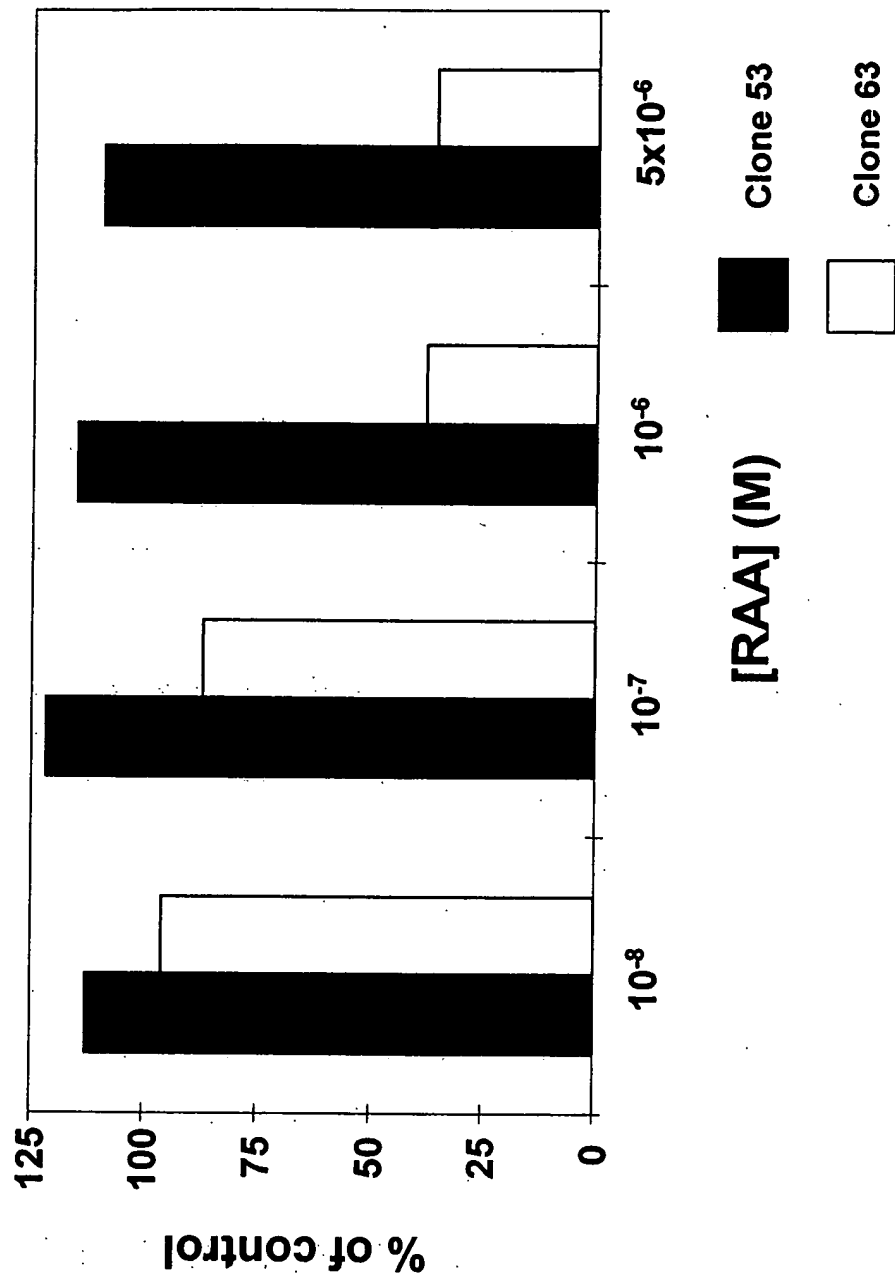
**FIGURE 3 B**



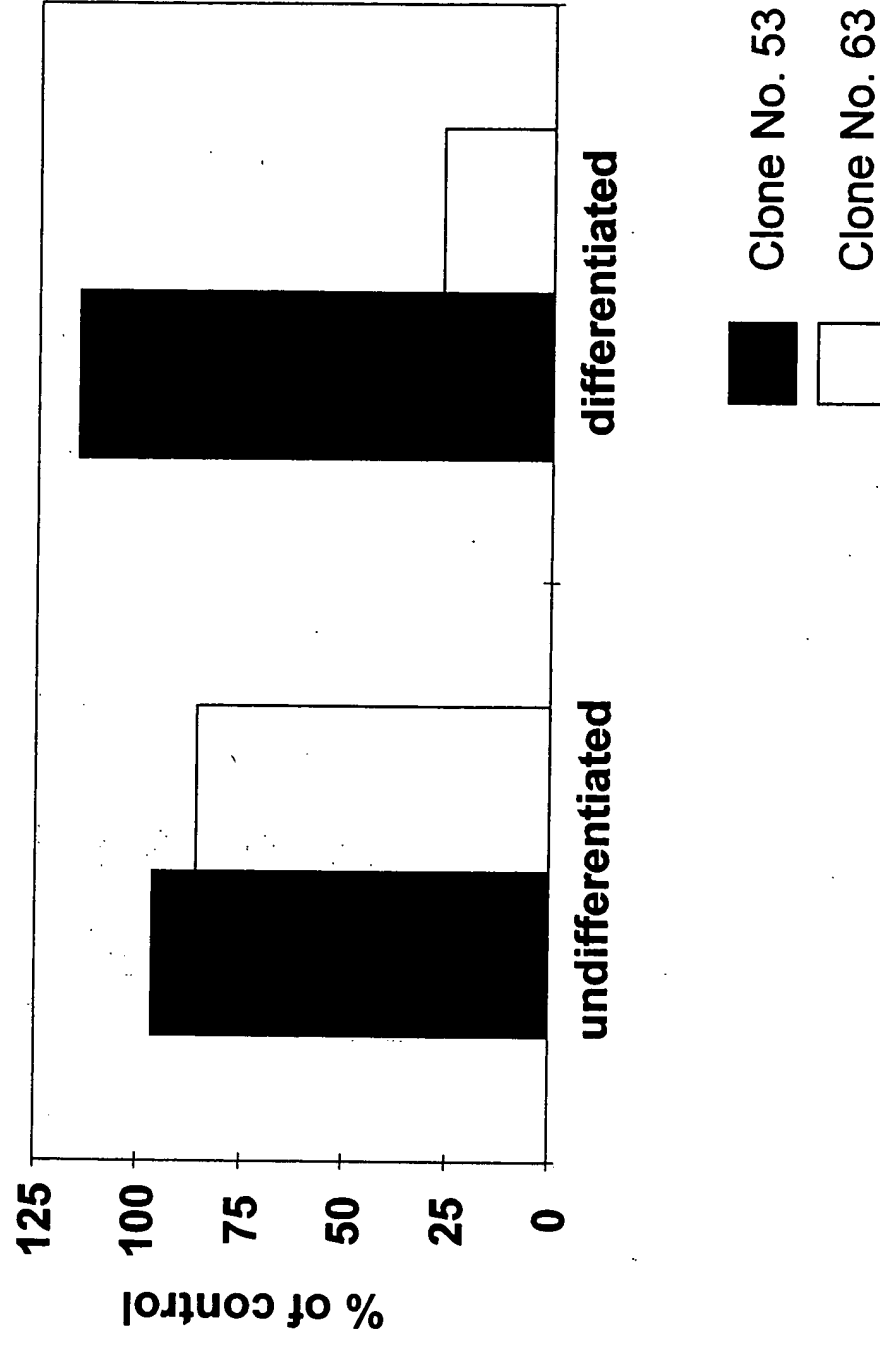
**FIGURE 4**



**FIGURE 5**



**FIGURE 6**



**FIGURE 7**



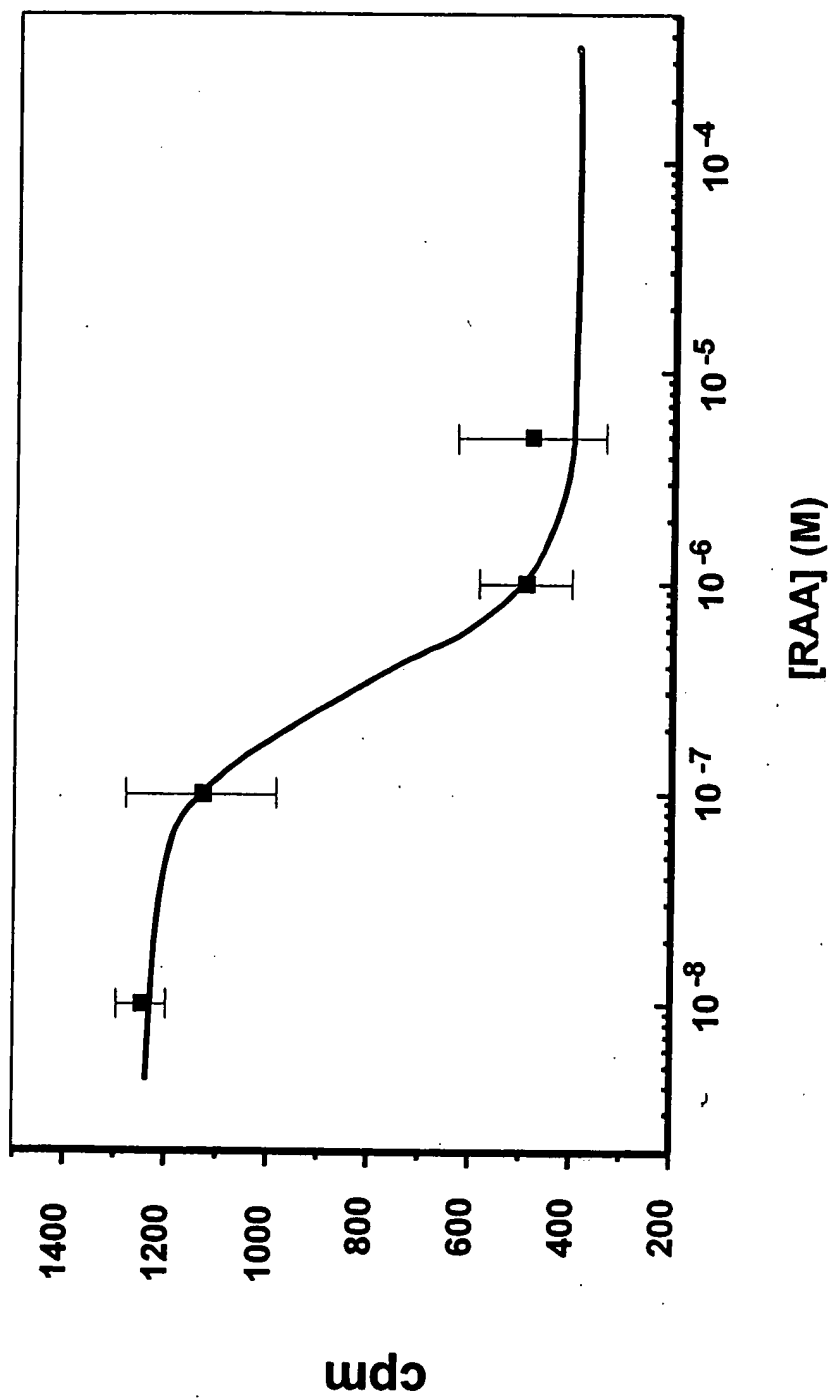


FIGURE 8

APP construct: 

- AUUUA {Bold/Underline}
- ☆ potential polyA signal sequence {Bold/Italics}
- Restriction Sites {Bold}

NotI

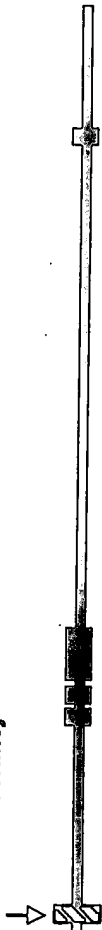
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1  GCGGCGGCCA CAGCAGCCTC TGAAGTTGGA CAGCAAAACC ATTGCTTCAC TACCCATCGG TGTCATTTA TAGAATAATG TGGGAAGAAA CAAACCCGTT
101 TTATGATTTA CTCATTATCG CCTTTTGACA GCTGTGCTGT AACACAACTA GATGCCTGAA CTTGAAATTA TCCACACATC AGTAATGTAT TCTATCTCTC
201 TTTACATTTT GGTCTCTATA CTACATTATT AATGGGTTTT GTGTACTGTA AAGAAATTAG CTGTATCAA CTAGTGCATG AATAGATTCT CTCCTGATTA
301 TTTATCACAT AGCCCCCTTAG CCAGTTGTAT ATTATTCTTG TGGTTTCTGA CCCAATTAAG TCCTACTTTA CATATGCTTT AGAATCGAT GGGGGATGCT
401 TCATGTGAAC GTGGGAGTTC AGCTGCTTCT CTTCCTTAAG TATTCCTTTC CTGATCACTA TGCATTTTAA AGTTAAACAT TTTTAAGTAT TTCAGATGCT
501 TTAGAGAGAT TTTTTTTTCC ATGACTGCAAT TTTACTGTAC AGATTGCTGC TTCGTCTATA TTTGTGATAT AGGAATTAAG AGGATACACA CGTTTGTTC
601 TTCGTGCCCTG TTTTATGTGC ACACATTAGG CATTGAGACT TCAAGCTTTT CTTTTTTTGT CCACGTATCT TTGGGTCTTT GATAAAGAAA AGAATCCCTG
701 TTCATTGTAA GCACTTTTAC GGGGCGGGTG GGGAGGGGTG CTCTGCTGGT CTTCAATTAC CAAGAATTCT CCAAAACAAT TTTCTGCAGG ATGATTGTAC
801 AGAATCATTG CTTATGACAT GATCGCTTTC TACACTGTAT TACATAAATA AATTAAATAA AATAACCCCG GGCAAGACTT TTTCTTGAAG GATGACTACA
901 GACATTAAAT AATCGAAGTA ATTTTGGGTG GGGAGAGAG GCAGATTCAA TTTTCTTTAA CCAGTCTGAA GTTTCATTTA TGATACAAAA GAAGATGAAA
1001 ATGGAAGTGG CAATATAAGG GGATGAGGAA GGCATGCCCTG GACAACCCT TCCTTTAAGA TGTGCTTCA ATTTGTATAA AATGGTGTTC TCATGTAGCG
1101 GCGGC
NotI
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FIGURE 9

Length: 1105 bp

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stop codon {***Bold/Italics/Underline***}



□ AUUUA {**BOLD/Underline**}  
Restriction Sites {**BOLD**}

**Not**

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1  GCGSCGCTG AAGTCAACAT GCCTGCCCA AACAAATATG CAAAGGTTT ACTAAGCAG TAGAATAAT ATGATTGTC AGTGATGAC CATGAACAA
101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA CAGACAGACA CAACAATTAA CAGTCTTCAG GCAAAACGTC
201 GAATCAGCTA TTTACTGCCA AAGGGAATA TCATTTATTT TTTACATTAT TAAGAAAAAA AGATTATTT ATTTAGACA GTCCCATCAA AACTCCTGTC
301 TTTGGAAATC CGACCACTAA TTGCCAAGCA CCGCTTCGTG TGGCTCCACC TGGATGTTCT GTGCCTGTAA ACATAGATTG GCTTTCCATG TTGTTGGCCG
401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGGTGT TCATTCACCT
501 GAATTTCTTT GCCCTGGGG CTGTGATATT AACAGAGGGA GGGTTCCTGT GGGGGGAAGT CCATGCCCTCC CTGGCCTGAA GAAGAGACTC TTTGCATATG
601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATGGGAAAA
701 ATGCCCTTAA ATCATAGGAA AGTATTTTTT TAAGCTACCA ATTGTGCCGA GAAAGCATT TTAGCAATTT ATACAATATC ATCCAGTACC TTAAGCCCTG
801 ATTGTGTATA TTCATATATT TTGGATACGC ACCCCCCAAC TCCCAATACT GGCTCTGTCT GAGTAAGAAA CAGATCCTC TGGAACTTGA GGAAGTGCGG
901 CCGC

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**Not**

Length: 904 bp

FIGURE 10

stop codon {***Bold/Italics/Underline***}



bcl-2 $\alpha$ -short construct:

■ AUUUA {***Bold/Underline***}  
Restriction Sites {***Bold***}

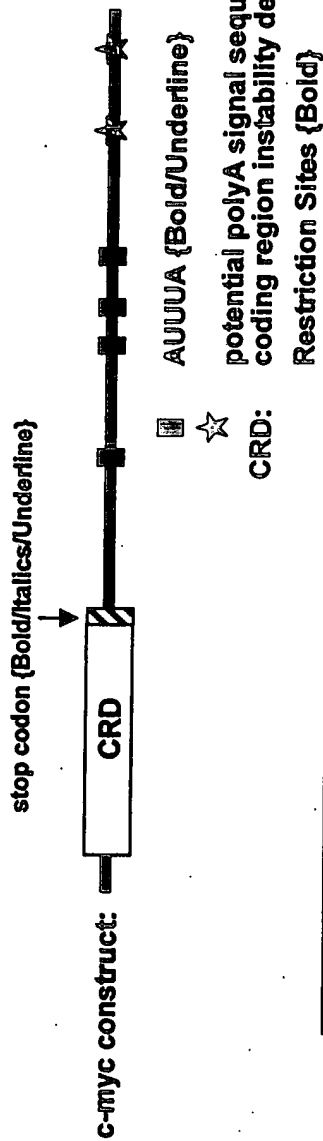
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NotI
1  GCGGCGGCTG AAGTCAACAT GCCTGCCCA ACAATATG CAAAAGGTTT
51  ACTAAGCAG TAGAATAAT ATGCATTGTC AGTGATGTAC CATGAACAA
101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA
151 CAGACAGACA CACACACACA CAACAATTAA CAGTCTTCAG GCAAAAGGTC
201 GAATCAGCTA TTTACTGCCA AAGGGAATA TCATTTATTT TTTACATTAT
251 TAAGAAAAAA AGATTATTTT ATTTAAGACA GTCCCATCAA AACTCCTGTC
301 TTTGGAATC CGACCACTAA TTGCCAAGCA CCGCTTCCTG TGGCTCCACC
351 TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG
401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG
451 AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGTGT TCATTCACTT
501 GCATTTCITT GCCCTGGGGG CTGTGATATT AACAGAGGGA GGGTCCCTGT
551 GGGGGGAAGT CCATGCCTCC CTGGCCTGAA GAAGAGACTC TTTGCATATG
601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT
651 GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATGGGAAAA
701 ATCGGCGCGC
NotI

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Length: 710 bp

FIGURE 11



	<b><u>NotI</u></b>
1	CGGCGGCTC GGAGCTTTTT TGCCCTGCGT GACCAGATCC CGGAGTTGGA
51	AAACAATGAA <u>AAGGCCCCCA</u> AGGTAGTTAT CCTTAAAAA GCCACAGCAT
101	ACATCCTGTC <u>CGTCCAAGCA</u> GAGGAGCAAA AGCTCAITTC TGAAGAGGAC
151	TTGTTGCGGA <u>AACGACGAGA</u> ACAGTTGAAA CACAAACTTG AACAGCTACG
201	GAACTCTTGT <u>GCGTAAGGAA</u> AAGTAAGGAA AACGATTCTT TCTGACAGAA
251	ATGTCCTGAG CAATCACCTA TGAACCTTGT TCAATGTCAT GATCAAAATGC
301	AACCTCACAA CCTTGGCTGA GTCTTGAGAC TGAAGATTT <u>AGCCATAATG</u>
351	TAAACTGCCT CAAATTGGAC TTTGGGCATA AAAGAACTTT TTTATGCTTA
401	CCATCTTTTT TTTTCTTTA ACAGATTGT <u>ATTTAAGAAT</u> TGTTTTAAA
451	AAATTTTAAG <u>ATTACACAA</u> TGTTTCTCTG TAAATATTGC CATTAAATGT
501	AAATPACTTT <u>AATAAAACGT</u> TTATAGCAGT TACACAGAAT TTCAATCCTA
551	GTATATAGTA CCTAGTATTA TAGGTACTAT AAACCCTAAT <u>TTTTTTTATT</u>
601	<u>TAA</u> GTACATT TTGCTTTTAA AAGTTGATTT TTTTCTATTG TTTTAGAAA
651	AAATAAATA ACTGGCAAT ATATCAITGA GGCATATG
	<b><u>NdeI</u></b>

Length: 688 bp

FIGURE 12

stop codon (***UAA***)

TNF- $\alpha$  construct:



■ AUUUA (***UAA***)

☆ Potential polyA signal sequence (***UAA***)

Restriction Sites (***UAA***)

	NotI
1	CGGCGGCTG AGGAGGACGA ACATCCAACC TTCCCAACG CCTCCCTGC CCCAATCCCT
61	TTATTACCCC CTCCTTCAGA CACCCTCAAC CTCCTCTGGC TCAAAAAGAG AATTGGGGG
121	TTAGGGTCGG AACCCAAAGCT TAGAACTTTA AGCAACAAGA CCACCACTTC GAAACCTGGG
181	ATTGAGGAAT GTGTGGCCTG CACAGTGAAG TGCTGGCAAC CACTAAGAAT TCAAACTGGG
241	GCCTCCAGAA CTCACTGGGG CCTACAGCTT TGATCCTGA CATCTGGAAT CTGGAGACCA
301	GGGAGCCTTT GGTCTGGCC AGAATGCTGC AGGACTTGAG AAGACCTCAC CTAGAAATTG
361	ACACAAGTGG ACCTTAGGCC TTCCTCTCTC CAGATGTTTC CAGACTTCCT TGAGACACGG
421	AGCCAGCCC TCCCCATGGA GCCAGCTCC TCTATTATG TTTGCACTTG TGATTATTGA
481	TTATTATTAT ATTATTATT TATTACAGA TGAATGTTT TATTGGGAG ACCGGGGTAT
541	CCTGGGGGAC CCAATGTAGG AGTGCCTTG GCTCAGACAT GTTTCCCGT AAAACGGAGC
601	TGAACAATAG GCTGTTCCCA TGTAGCCCC TGGCCTCTGT GCCTCTTTT GATTATGTTT
661	TTAAAATAT TTAATCTGAT AAGTTGTCTA AACAAATGCTG ATTGGTGAC CAACTGTCAC
721	TCATTGCTGA GCCTCTGCTC CCCAGGGGAG TTGTGCTGT AATCGCCCTA CTATTCAGTG
781	GCGAGAAATA AAGTTTGCTT CATATG

NdeI

Length: 806 bp

FIGURE 13

stop codon {***Bold/Italics/Underline***}

IL-18 construct:



■ AUUUA {***Bold/Underline***}

☆ Potential polyA signal sequence {***Bold/Italics***}

Restriction Sites {***Bold***}

Notl	
1	GCGGCGGCTA <u>AAGAGAGCTG</u> TACCCAGAGA GTCCTGTGCT GAATGGGAC
51	TCAATCCCTA GGGCTGGCAG AAAGGGAACA GAAAGTTTT TGAGTACGGC
101	TATAGCCTGG ACTTTCCTGT TGTCTACACC AATGCCCAAC TGCCTGCCTT
151	AGGCTAGTGC TAAGAGGATC TCCTGTCCAT CAGCCAGGAC AGTCAGCTCT
201	CTCCTTTCAG GGCCAATCCC CAGCCCTTTT GTTGAGCCAG GCCTCTCTCA
251	CCTCTCCTAC TCACTTAAAG CCCGCCCTGAC AGAACCACG GCCACATTTG
301	GTTCTAAGAA ACCCTCTGTC ATTGCTCCG ACATTCTGAT GAGCAACCGC
351	TTCCCTATTT <u>ATTATTTTAT</u> TTGTTTGTTT GTTTTATTCA TTGCTCTAAT
401	<u>TTATTCAAAG</u> GGGGCAAGAA GTAGCAGTGT CTGTAAGA GCTAGTTTTT
451	TAATAGCTAT GGAATCAATT CAATTTGGAC TGGTGTGCTC TCTTTAATC
501	AAGTCCTTTA ATTAAGACTG AAAATATATA AGCTCAGATT <u>ATTAAATGG</u>
551	GAATATTTAT <u>AAATGAGCAA</u> ATATCACTACT GTTCAATGGT TCTGAATAAA
601	ACTTCAACCAT ATG
	NdeI

Length: 613 bp

FIGURE 14

VEGF construct: 

■ AUUUA {Bold/Underline}

★ Potential polyA signal sequence {Bold/Italics}  
Restriction Sites {Bold}

	<b>NotI</b>
1	GGGGCCGCAT TGCTGTGCTT TGGGGATTCC CTCCACATGC TGCACGCCA TCTCGCCCC AGGGGCACTG CCTGGAAGAT TCAGGAGCCT GGGCGGCCTT
101	CGCTTACTCT CACCTGCTTC TGAGTTGCC AGGAGGCCAC TGGCAGATGT CCCGGCGAAG AGAAGAGACA CATTGTTGGA AGAAGCAGCC CATGACAGCT
201	CCCCCTCCTG GGACTCGCCC TCATCCTCTT CCGTCTCCCC TTCTTGGGT GCAGCCTAAA AGGAACATG TCCTCACACC ATTGAAACCA CTAGTTCTGT
301	CCCCCCAGGA GACCTGGTTG TGTGTGTGTG AGTGGTTGAC CTTCCTCCAT CCCCTGCTCC TTCCCAGGC ACAGAGAGAC AGGGCAGGAT
401	CCACGTGCCC ATTGTGGAGG CAGAGAAAAG AGAAAGTGT TTATATACGG TACTTATTTA ATATCCCTTT TTAATTAGAA ATTAAAACAG TTAATTTAAT
501	TAAAGAGTAG GGTTTTTTTT CAGTATTCTT GGTAAATATT TAATTTCAAC TATTTATGAG ATGTATCTTT TGCTCTCTCT TGTCTCTTA TTTGTACCGG
601	TTTTTGTATA TAAAAATCAT GTTCCAATC TCTCTCTCCC TGATCGGTGA CAGTCACTAG CTTATCTTGA ACAGATATTT AATTTTGCTA ACACTCAGCT
701	CTGCCCTCCC CGATCCCCTG GCTCCCCCAGC ACACATTCCT TTGAATAAAG GTTCAATAT ACACTACAT ACTATATATA TATATTTGGC AACTTGTATT
801	TGTGTGTATA TATATATATA TATGTTTATG TATATATGT ATTCTGATAA AATAGACATT GCTATTCTGT TTTTATATG TAAAAACAAA ACAAGAAAAA
901	ATAGAGAATT CTACATACTA AATCTCTCTC CTTTTTTTAA TTTAATATTT GTTATCATTT ATTATATGGT GCTACTGTTT ATCCGTAATA ATTGTGGGA
1001	AAAGATATTA ACATCAGGTC TTTGTCTCTA GTGCAGTTTT TCGAGATATT CCGTAGTACA TATTTATTTT TAAACAACGA CAAAGAAATA CAGAACAATAT
1101	<b>G</b> <b>NdeI</b>

Length: 1101 bp

FIGURE 15

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VEGF 3'UTR hypoxia domain construct:



■ AUUUA {Bold/Underline}  
Restriction Sites {Bold}

**NotI**

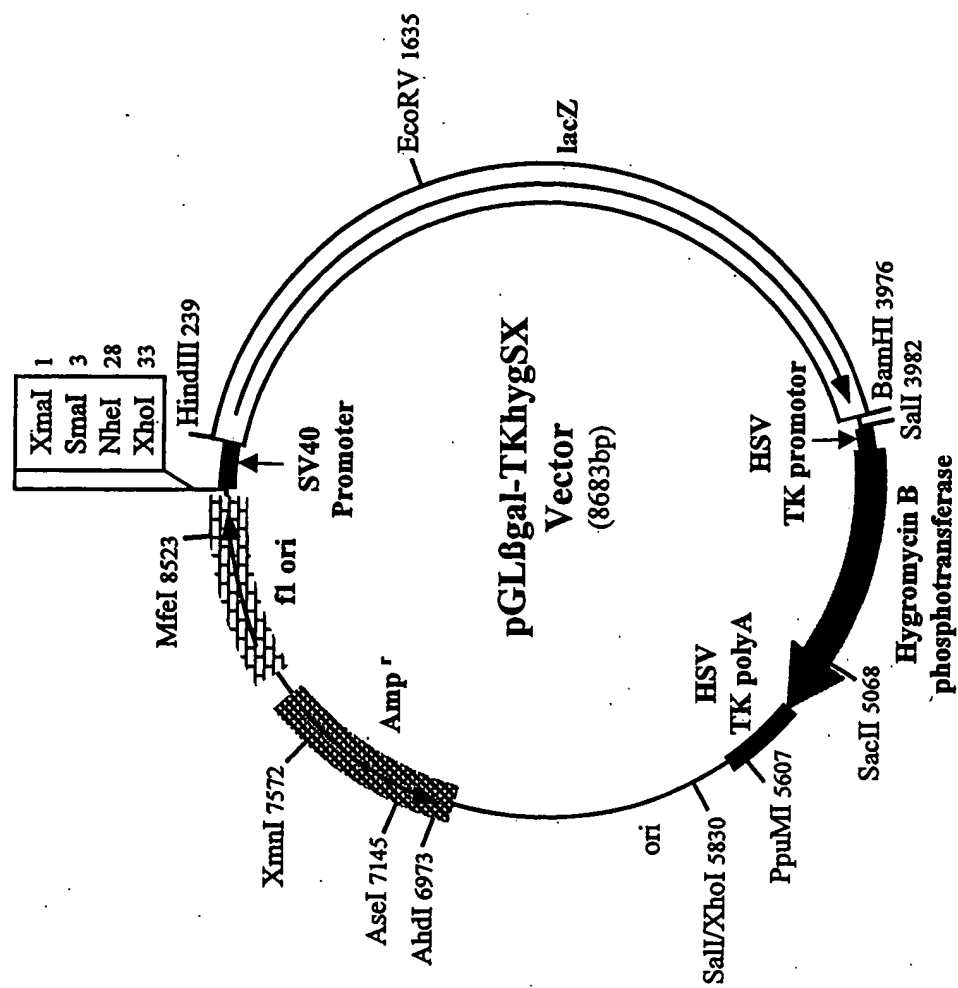
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1  GCGGCCGCAT TCCTGTAGAC ACACCCACCC ACATACATAC ATTTATATAT
51  ATATATATTA TATATATATA AAAATAAATA TCTCTATTTT ATATATATAA
101 AATATATATA TTCTTTTTTT AAATTAACAG TGCTAATGTT ATTGGTGTCT
151 TCACTGGATG AACATATG
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**NdeI**

Length: 168 bp

**FIGURE 16**

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**FIGURE 17**